26. (Original). A recombinant nucleic acid molecule, comprising a promoter sequence operably linked to the nucleic acid molecule of claim 24.

27. (Original). A cell transformed with a recombinant nucleic acid molecule according to claim 26.

Please cancel claims 1, 9, 16, 18, 23 and 25 without prejudice.

In the Drawings:

Please replace Figure 4 with the enclosed substitute Figure 4.

A clean, substitute copy of Figure 4 and a copy showing the changes are attached.

Please replace Figure 6A-N with the enclosed substitute Figure 6A-6N.

A clean, substitute copy of Figure 6A-6N and a copy showing the changes are attached.

In the Sequence Listing:

Please replace the current Sequence Listing with the enclosed replacement Sequence Listing.

REMARKS

Claims 1, 3-6, 8-11, 14, 16, 18, and 23-27 are the subject of the Office action. Claims 1, 9, 18, and 23 are cancelled as drawn to non-elected groups. Claims 16 and 25 are also cancelled, and claims 3, 4, 8, 14, and 24 are amended. Applicants expressly reserve the right to pursue protection of any or all of the subject matter of the cancelled claims in a subsequent application.

In addition, a new title has been provided, sixteen paragraphs have been added to the specification, 35 paragraphs of the specification have been amended, the abstract has been amended, and the Sequence Listing, Figure 4, and Figure 6A-N have been replaced.

Support for the amendment to the Figure 1 legend (in the specification at page 8, lines 5-10) may be found in the specification, *e.g.*, at page 2, line 7 through page 3, line 1. Otherwise, support for the foregoing amendments is discussed below where appropriate. No

new matter is introduced by these amendments. Unless specifically stated otherwise, none of these amendments is intended to limit the scope of any claim.

After entry of this amendment **claims 3-6, 8, 10, 11, 14, 24, 26, and 27 are pending in this application.**

Applicant's Election of SuperGroup B

Applicants thank the Examiner for (i) acknowledging Applicants' election of SuperGroup B directed to claims 3-6, 8, 10, 11, 14, 16, and 24-27 as they relate to TAX6 (SEQ ID NOs: 44 and 45), and (ii) identifying Group XXXV as the group that properly corresponds to the stated election.

Applicants' reference to "Group XV" in the Response to Restriction Requirement, dated October 23, 2003 ("Restriction Response"), was a clerical error. As the Examiner recognized, the Restriction Response should have referred to "Group XXXV" directed to claims from SuperGroup B related to SEQ ID NOs: 44 and 45.

As noted above, SuperGroup B includes claims 3-6, 8, 10, 11, 14, 16, ***and 24-27***. The Office action states (at line 4(a) of the Office Action Summary) that claims 24-27 are withdrawn from consideration. It also appears that such claims have not been examined. Applicants traverse the withdrawal of claims 24-27 from examination. Claims 24-26 are included in the elected SuperGroup B, and Applicants request examination of amended claims 24, 26 and 27 which are still pending in this application.

Compliance with the Sequence Rules

Figure 4 has been corrected to comply with the rules for sequence disclosures and to clarify which nucleic acid or amino acid sequence corresponds to which sequence identifier. Specifically, sequence identifiers are now shown for the amino acid sequences in Figure 4 (*i.e.*, residues 1-7 of SEQ ID NO: 30, residues 4-10 of SEQ ID NO: 30, SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41). For clarity purposes, each nucleic acid sequence identifier (*i.e.*, SEQ ID NOs: 34-38) has been moved to the same line as the corresponding primer name.

In further compliance with the rules for sequence disclosures, the amino acid sequences referred to in Table 1 have been identified by the applicable sequence identifiers.

Several readily discernible errors in the Sequence Listing also have been corrected so as to comply with the sequence rules. Specifically, SEQ ID NOs: 34-38 of the Sequence Listing have been corrected to properly correspond to the nucleic acid sequences shown, *e.g.*, in original Figure 4. In addition, SEQ ID NO: 65 of the Sequence Listing has been corrected to show the amino acid sequence of protein "aac17079," which is set forth, *e.g.*, in Figure 6A-6N and in original Table 1 (see, Protein Identification No. g3152598).

Applicants submit herewith a replacement electronic copy (diskette) of the Sequence Listing, and a corresponding paper copy (91 pages). In compliance with 37 C.F.R. § 1.821(f), the undersigned declares that the nucleotide sequences presented in the paper copy of the Sequence Listing submitted herewith are the same as the sequences contained in the computer-readable form of the Sequence Listing.

Objections to the Specification

The specification has been objected to for allegedly being confusing because SEQ ID NOs: 61-74 are not mentioned in the specification and/or claims. Applicants traverse this objection. SEQ ID NOs: 61-74 are described in Figure 6A-6N. By this amendment, Applicants also add brief descriptions of SEQ ID NOs: 61-74 in the specification. Thus, Applicants request that this objection be withdrawn.

Errors in Figure 6A-6N: In preparing the response to the foregoing objection, readily discernible errors in some of the Figure 6A-6N labels were noted. A comparison of the original Sequence Listing with the amino acid sequences shown in Figure 6A-6N clearly demonstrates that the proteins identified as "aab61522," "cab10319," and "cab40761" correspond to SEQ ID NOs: 59, 60, and 61, respectively, in the original Sequence Listing. The appropriate labels in Figure 6A-6N were corrected accordingly. In addition, a typographical error in the label "aab95293" of Figure 6A-6N was corrected to "abb9528**3**" (emphasis added). This correction is

supported at least by the description of Figure 6A-6N (at page 9, lines 20-24) and by Table 1 (see, Protein Identification No. g2213628).

The specification has been objected to for allegedly lacking updated continuity data. Applicants have amended the specification to add the continuity data, as suggested by the Examiner. Applicants thank the Examiner for the suggestions in this regard, and request that this objection be withdrawn.

The specification has been objected to because the title allegedly is not descriptive. Applicants traverse this objection. However, to facilitate prosecution of the application, Applicants have amended the title as suggested by the Examiner, and request that this objection be withdrawn.

The abstract has been objected to for allegedly not completely describing the disclosed subject matter. Applicants traverse this objection. The abstract clearly describes the *disclosed* subject matter, as required by 37 C.F.R. §1.72 and as set forth in MPEP §608.01(b). Neither the foregoing rule nor its MPEP guideline requires that the abstract describe the *claimed* subject matter, which is what the Examiner appears to be requiring. However, to facilitate prosecution of the application, the abstract has been amended in part as suggested by the Examiner. On the basis of this argument and amendment, Applicants request that this objection be withdrawn.

The specification has been objected to for alleged inappropriate notation of an internet address. The specification has been amended to remove the references to the internet addresses identified by the Examiner. Therefore, Applicants request that this objection be withdrawn.

The specification has been objected to for allegedly containing confusing characters. Occurrences of the backwards "E" and the upside-down "A" in the specification have been corrected to read "β" and "α," respectively. The correct characters are discernible from the context of the words containing the incorrect characters. Applicants request that this objection be withdrawn.

The specification has been objected to for allegedly being confusing in its varied use of names for TAX6 enzyme. Applicants traverse this objection.

The specification clearly defines "transacylase" and its synonym "acyltransferase," *e.g.*, at page 15, line 27 through page 16, line 5). TAX6 transfers an acyl group (*e.g.*, acetyl) to a reactant (see, *e.g.*, page 34, line 32 through page 35, line 12 of the specification). Therefore, TAX6 is properly named a transacylase or acyltransferase. Specifically, TAX6 has been named 10-deacetylbaccatin III-10-*O*-acetyl transferase. It is not uncommon or confusing to describe an item by two related terms; for instance, by the name of an enzyme and by the class of enzymes to which the named enzyme belongs. An analogy in common parlance is, *e.g.*, "Lassie" is a Collie. Someone describing Lassie would be correct to call the dog either by its name or to call it a Collie or to call it a dog. Applicants suggest that such usage is not confusing in this day-to-day example or in relation to TAX6.

With regard to the term "acyltransacylase," Applicants believe the specification is also clear with respect to the meaning of this term as it relates to TAX6. However, to facilitate prosecution of the application, Applicants have amended the specification to substitute the term "acyltransferase" for the term "acyltransacylase."

Based on the foregoing arguments and amendments, Applicants request that this objection be withdrawn.

Claim Objections

Claims 3-6 have been objected to for depending from a non-elected claim. Claim 3 has been amended to remove its dependency from any other claim. Amended claim 4 and claims 5 and 6 each depend from claim 3 (directly or indirectly), which is an elected claim. Therefore, this objection is moot and Applicants request that it be withdrawn.

Claim 16 has been objected to for depending from a cancelled claim. Claim 16 has been cancelled by this amendment. Thus, this objection is moot and Applicants request that it be withdrawn.

Claims 3-6, 8, 10, 11, and 14 are objected to for containing non-elected subject matter. Claims 3, 4, 8, and 14 (and, therefore, claims that depend from them, *i.e.*, claims 5, 6, 10, and 11) have been amended to remove non-elected subject matter. Therefore, this objection is moot and Applicants request that it be withdrawn.

Claim Rejections under 35 U.S.C. §112, 2nd paragraph:

Claims 8, 10, 11, 14, and 16 have been rejected under 35 U.S.C. §112, 2nd paragraph because the term "transacylase" allegedly is unclear when used with respect to TAX6. Applicants traverse this rejection. As discussed above in connection with the objection to the specification for allegedly being confusing in its varied use of names for TAX6 enzyme, the meaning of the term "transacylase" with regard to TAX6 is clear and is clearly described in the specification. On the basis of the arguments made previously, Applicants request that this claim objection be withdrawn.

Claim Rejections under 35 U.S.C. §112, 1st paragraph:

Claims 8, 10, and 11 stand rejected under 35 U.S.C. §112, 1st paragraph, written description because allegedly the "hybridizing language, by virtue of the fragment language, does not impart a definite structure for the claimed nucleic acid molecules[, and] the functional language does not impart a clear function." Applicants traverse this rejection.

To facilitate prosecution of the application, however, Applicants have abided the Examiner's suggestions at ¶17 on page 8 of the Office action. Claim 8 has been amended to remove the phrase "fragments thereof," and to recite that the isolated nucleic acid molecule "encodes a protein having transacylase activity, wherein the protein uses as a substrate a taxoid with a 10-hydroxyl group." Support for the substrate language is found in the specification, for example, at page 24, lines 14-17.

Applicants thank Examiner Kerr for her suggestions for obviating this rejection, and request that the rejection be withdrawn.

Claim 14 stands rejected under 35 U.S.C. §112, 1st paragraph, written description because the claim allegedly does not recite a clear function. Applicants traverse this rejection. However, to facilitate prosecution of the application, Applicants have amended claim 14 in conformance with the Examiner's suggestion (in ¶18 on page 9 of the Office action). Support for this claim 14 amendment is discussed above (see rejection of claims 8, 10, and 11 under §112, ¶1, written description). Applicants thank the Examiner for her suggestion, and request that this rejection of claim 14 be withdrawn.

Claims 8, 10, 11, and 14 stand rejected under 35 U.S.C. §112, 1st paragraph, scope of enablement because the specification allegedly does not "provide enablement for nucleic acid molecules having 60% sequence identity (or hybridizing under low stringency conditions) with SEQ ID NO: 44." Applicants traverse this rejection.

Examiner Kerr states at ¶19 on page 9 of the Office action that the specification is enabling for nucleic acid molecules having 90% sequence identity (or hybridizing under very high stringency conditions) with SEQ ID NO: 44. To facilitate prosecution of this application, Applicants have amended claim 8 to recite, in relevant part, "[a]n isolated nucleic acid molecule that...hybridizes under very high stringency conditions with a nucleic acid sequence as set forth in SEQ ID NO: 44," and have amended claim 14 to recite, in relevant part, "[a]n isolated nucleic acid molecule that...has at least 90% sequence identity with a nucleic acid sequence as set forth in SEQ ID NO: 44."

In accordance with the Examiner's finding of enablement, Applicants believe these amendments render claim 8 (and its dependent claims 10 and 11) and claim 14 allowable as being fully enabled by the disclosure, and therefore request that this rejection be withdrawn.

Claim Rejections under 35 U.S.C. §102(b):

Claim 8 stands rejected under 35 U.S.C. §102(b) as being allegedly anticipated by GenBank Accession Number X66785, a nucleotide sequence that encodes a transacylase, particularly dihydrolipoyl transacylase (E2). Applicants traverse this rejection.

The Examiner explains this rejection with the single argument that "the sequence limitations [of claim 8] require no definite structure since all probes comprise 'a fragment' of SEQ ID NO: 44, a fragment being as small as a single nucleotide." As discussed above, claim 8 has been amended to remove the phrase "fragments thereof." Thus, the basis of this §102(b) rejection has been rendered moot. Accordingly, Applicants request that this rejection be withdrawn.

Claim Rejections under 35 U.S.C. §103(a):

Claims 8, 10, 11, and 14 stand rejected under 35 U.S.C. §103(a) as allegedly being obvious in light of Menhard *et al.*, *Phytochemistry*, 50:763-774, March 1999 ("Menhard") or Zocher *et al.*, *Biochem. Biophys. Res. Comm.*, 229:16-20, 1996 ("Zocher"), either in view of GenBank Accession Number AF456342; Matsudaira, *Meth. Enzymol.*, 182:602-613, 1990 ("Matsudaira"); Wozney, *Meth. Enzymol.*, 182:738-751, 1990 ("Wozney"); or Maniatis *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, 1982 ("Maniatis"). Applicants traverse this rejection. In particular, Applicants traverse the Examiner's reliance on Menhart, which was published less than one year before the priority date of claims 8, 10, 11, and 14.

To establish a *prima facie* case of obviousness, the Examiner must identify all of the claimed elements in one or more prior art references and provide a motivation or suggestion to combine or modify the prior art references coupled with a reasonable expectation of success (MPEP §2143). The teaching or suggestion to make the claimed combination and the reasonable expectation of success must both be found in the prior art, not in the Applicants' disclosure (MPEP §2143).

The Examiner points out that "[n]either Menhard nor Zocher teach the protein sequence or encoding DNA sequence of their [respective] acetyltransferases" (see, ¶21 on page 12 of the Office action). In contrast, claims 8, 10, 11, and 14 each recite particular isolated nucleic acid molecules. None of these sequences is taught or suggested by Menhard or Zocher. Furthermore, none of the secondary references (*i.e.*, Matsudaira, Wozney, and Maniatis) discloses these sequences either. Because the references cited by the Examiner fail to teach or suggest, alone or

in combination, all the elements of the subject claims, such references cannot serve as the basis of a rejection of the claims under 35 U.S.C. §103(a).

Even if, for the sake of argument (and not making any admissions), the cited references collectively discussed all the claimed elements, there is no motivation or suggestion to the ordinarily skilled person to combine the references in an effort to derive the subject claims. As the Office action states (see, ¶21 at page 13 of the Office action), Menhard or Zocher in light of Matsudaira, Wozney, or Maniatis must teach an ordinarily skilled artisan to combine an extraordinary number of extraordinarily complex steps. Specifically, the ordinarily skilled artisan would have had to isolate a protein solution having acetyltransferase activity (such as Menhard or Zocher) and then (i) obtain a partial amino acid sequence from an isolated polypeptide, (ii) synthesize a degenerate polynucleotide probe based on the partial amino acid sequence, (iii) use the polynucleotide probe to screen a cDNA or genomic DNA library to identify a full-length cDNA or genomic clone, (iv) construct expression vectors comprising the isolated cDNA or genomic clones, and (v) transform a host cell with an expression vector comprising the isolated cDNA or genomic clone. The Examiner contends that each of steps (i) – (v) is taught by Matsudaira, Wozney, and Maniatis individually. But, in fact, all five of these steps are not taught by any single reference.

Nothing in any of the cited references teaches the particular combination of steps recited by the Examiner, or suggests pursuing the steps in this particular order. Any suggestion or motivation to combine the references to derive the subject claims is only found by reference to Applicants' disclosure. This type of hindsight is impermissible and cannot support an obviousness rejection.

Finally, even if an ordinarily skilled artisan were motivated to combine the cited references in the manner described above, there certainly would be no reasonable expectation of success. One knowledgeable in the art can imagine numerous pitfalls in any one of the steps set forth above. For example, the "purified" acetyltransferase of Menhard or Zocher may not have been sufficiently pure to obtain protein sequence information sufficiently accurate for designing useful probes. Furthermore, even accurate protein sequence information does not automatically

give rise to useful probes (see, *e.g.*, page 18 of the specification). Moreover, Applicants' specification specifically teaches that not every pair of degenerate primers designed by Applicants was useful for identifying the transacylases disclosed in the specification (see, *e.g.*, Table 2). The foregoing are just a few examples of many potential problems that could be detailed. If molecular biological and protein purification techniques and the design of experiments employing such techniques were as simple as implied by the Office action, then any nucleic acid sequence would be rendered obvious for patentability purposes as soon as the enzyme activity of a "purified" protein was measured *in vitro*. This is not the correct standard of obviousness.

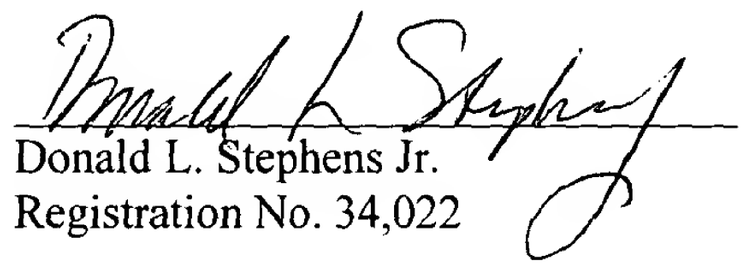
Based on any or all of the foregoing arguments, Applicants request that the rejection of claims 8, 10, 11, and 14 under 35 U.S.C. §103(a) be withdrawn.

CONCLUSION

It is respectfully submitted that the present claims are in a condition for allowance. If it may further issuance of these claims, the Examiner is invited to call the undersigned at the telephone number listed below.

Respectfully submitted,

KLARQUIST SPARKMAN, LLP

By 
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Marked-up Version of Amended Claims and Specification
Pursuant to 37 C.F.R. §§ 1.121(b)-(c)

In the Specification:

At page 1, lines 8-9:

This application is a divisional of ~~co-pending~~ U.S. Application No. 09/457,046, filed December 7, 1999, now issued as U.S. Patent No. 6,287,835, herein incorporated by reference, which is a continuation in part of ~~co-pending~~ U.S. Application No. 09/411,145, filed September 30, 1999, now abandoned, herein incorporated by reference.

At page 2, lines 23-28:

The second specific step of Taxol™ biosynthesis is an oxygenation reaction catalyzed by taxadiene-5~~∀~~-α-hydroxylase (**Figure 1**). The enzyme, characterized as a cytochrome P450, has been demonstrated in *Taxus* microsome preparations to catalyze the stereospecific hydroxylation of taxa-4(5),11(12)-diene, with double bond rearrangement, to taxa-4(20),11(12)-dien-5~~∀~~-α-ol (Hefner et al., *Chem. Biol.* **3**:479-489, 1996).

At page 2, line 29 through page 3, line 16:

The third specific step of Taxol™ biosynthesis appears to be the acetylation of taxa-4(20),11(12)-dien-5~~∀~~-α-ol to taxa-4(20),11(12)-dien-5~~∀~~-α-yl acetate by an acetyl CoA-dependent transacetylase (Walker et al., *Arch. Biochem. Biophys.* **364**:273-279, 1999), since the resulting acetate ester is then further efficiently oxygenated to a series of advanced polyhydroxylated Taxol™ metabolites in microsomal preparations that have been optimized for cytochrome P450 reactions (**Figure 1**). The enzyme has been isolated from induced yew cell cultures (*Taxus canadensis* and *Taxus cuspidata*), and the operationally soluble enzyme was partially purified by a combination of anion exchange, hydrophobic interaction, and affinity chromatography on immobilized coenzyme A resin. This acetyl transacylase has a pI and pH optimum of 4.7 and 9.0, respectively, and a molecular weight of about 50,000 as determined by gel-permeation chromatography. The enzyme shows high selectivity and high affinity for both cosubstrates with K_m values of 4.2 μM and 5.5 μM for taxadienol and acetyl CoA, respectively. The enzyme does not acetylate the more advanced Taxol™ precursors, 10-deacetylbaccatin III or

baccatin III. This acetyl transacylase is insensitive to monovalent and divalent metal ions, is only weakly inhibited by thiol-directed reagents and Co-enzyme A, and in general displays properties similar to those of other *O*-acetyl transacylases. This acetyl CoA:taxadien-5~~∀~~-α-ol *O*-acetyl transacylase from *Taxus* (Walker et al., *Arch. Biochem. Biophys.* **364**:273-279, 1999) appears to be substantially different in size, substrate selectivity, and kinetics from an acetyl CoA:10-hydroxytaxane *O*-acetyl transacylase recently isolated and described from *Taxus chinensis* (Menhard and Zenk, *Phytochemistry* **50**:763-774, 1999).

At page 3, lines 17-20:

Acquisition of the gene encoding the acetyl CoA:taxa-4(20),11(12)-dien-5~~∀~~-α-ol *O*-acetyl transacylase that catalyzes the first acylation step of Taxol™ biosynthesis and genes encoding other acyl transfer steps would represent an important advance in efforts to increase Taxol™ yields by genetic engineering and *in vitro* synthesis.

At page 6, lines 5-6:

SEQ ID NO: 25 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX2.

At page 6, lines 7-8:

SEQ ID NO: 26 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX2.

At page 6, lines 9-10:

SEQ ID NO: 27 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX1.

At page 6, lines 11-12:

SEQ ID NO: 28 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX1.

At page 7, lines 7-8:

SEQ ID NO: 44 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX6.

At page 7, lines 9-10:

SEQ ID NO: 45 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX6.

At page 7, lines 14-15:

SEQ ID NO: 49 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX5.

At page 7, lines 16-17:

SEQ ID NO: 50 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX5.

At page 7, lines 18-19:

SEQ ID NO: 51 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX7.

At page 7, lines 20-21:

SEQ ID NO: 52 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX7.

At page 7, lines 22-23:

SEQ ID NO: 53 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX10.

At page 7, lines 24-25:

SEQ ID NO: 54 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX10.

At page 7, lines 26-27:

SEQ ID NO: 55 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX12.

At page 7, lines 28-29:

SEQ ID NO: 56 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX12.

At page 7, lines 30-31:

SEQ ID NO: 57 is the nucleotide sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX13.

At page 8, lines 1-2:

SEQ ID NO: 58 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~acyltransferase clone TAX13.

At page 8, lines 5-10:

Figure 1: Enzymatic reactions of the Taxol™ pathway indicating cyclization of geranylgeranyl diphosphate to taxa-4(5),11(12)-diene (not shown), followed by hydroxylation/ and double bond rearrangement to form taxa-4(2), 11(12)-dien-5α-ol, followed by ~~and~~ acetylation to taxa-4(20),11(12)-dien-5α-yl acetate. The acetate is further converted to 10-deacetylbaccatin III, baccatin III, and Taxol™. In the figure, "a" denotes the activities of taxadiene synthase and taxadiene-5α-hydroxylase (in that order); "b" denotes ~~taxadiene-5α-hydroxylase; "c" denotes~~ taxadien-5α-ol acetyl transacylase; and "~~d~~c" – "e" denotes several subsequent steps.

At page 9, lines 1-18:

Figure 5 shows data obtained from a coupled gas chromatographic-mass spectrometric (GC-MS) analysis of the biosynthetic taxadien-5α-yl acetate formed during the incubation of

taxadien-5α-ol with soluble enzyme extracts from isopropyl β-D-thiogalactoside (IPTG)-induced *E. coli* JM109 cells transformed with full-length ~~acyltransacylase~~ acyltransferase clones TAX1 and TAX2. Panels **A** and **B** show the respective GC and MS profiles of authentic taxadien-5α-ol; panels **C** and **D** show the respective GC and MS profiles of authentic taxadien-5α-yl acetate; panel **E** shows the GC profile of taxadien-5α-ol (11.16 minutes), taxadien-5α-yl acetate (11.82 minutes), dehydrated taxadien-5α-ol ("TOH-H_2O" peak), and a contaminant, bis-(2-ethylhexyl)phthlate ("BEHP" peak, a plasticizer, CAS 117-81-7, extracted from buffer) after incubation of taxadien-5α-ol and acetyl coenzyme A with the soluble enzyme fraction derived from *E. coli* JM109 transformed with the full-length clone TAX1. Panel **F** shows the mass spectrum of biosynthetically formed taxadien-5α-yl acetate by the recombinant enzyme (11.82 minute peak in GC profile Panel E); panel **G** shows the GC profile of the products generated from taxadien-5α-ol and acetyl coenzyme A by incubation with the soluble enzyme fraction derived from *E. coli* JM109 cells transformed with the full-length clone TAX2 (note the absence of taxadien-5α-yl acetate indicating that this clone is inactive in the transacylase reaction).

At page 15, lines 9-16:

The National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST™, Altschul et al.. *J. Mol. Biol.* **215:**403-410, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence-analysis programs blastp, blastn, blastx, tblastn and tblastx. BLAST™ can be accessed ~~on the internet~~ at ~~http://www.ncbi.nlm.nih.gov/BLAST/~~the NCBI online site under the "BLAST" heading. A description of how to determine sequence identity using this program is available ~~on the internet~~ at ~~http://www.ncbi.nlm.nih.gov/BLAST/blast_help.html~~the NCBI online site under the "BLAST" heading and "BLAST overview" subheading.

At page 16, lines 26-33:

Biochemical studies have indicated that the third specific intermediate of the Taxol™ biosynthesis pathway is taxa-4(20),11(12)-dien-5~~∀~~ α-yl acetate, because this metabolite serves as a precursor of a series of polyhydroxy taxanes en route to the end-product (Hezari and

Croteau, *Planta Medica* **63**:291-295, 1997). The responsible enzyme, taxadienol acetyl transacylase, that converts taxadienol to the C5-acetate ester is, thus, an important candidate for cDNA isolation for the purpose of overexpression in relevant producing organisms to increase Taxol™ yield (Walker et al., *Arch. Biochem. Biophys*. **364**:273-279, 1999).

At page 19, line 7:

Accession No. (Seq. Identifier)	**Protein Identification No.**	**Function**
AC000103_AT (SEQ ID NO: 59)	g2213627	unknown; from genomic sequence for *Arabidopsis thaliana* BAC F21J9
AC000103_AT (SEQ ID NO: 62)	g2213628	unknown; from genomic sequence for *A. thaliana* BAC F21J9
AF002109_AT (SEQ ID NO: 63)	g2088651	unknown; hypersensitivity-related gene 201 isolog
AC002560_AT (SEQ ID NO: 64)	g2809263	unknown; from genomic sequence for *A. thaliana* BAC F21B7
AC002986_AT (SEQ ID NO: 65)	g3152598	unknown; similarity to C2-HC type zinc finger protein C.e-MyT1 gb/U67079 from *C. elegans* and to hypersensitivity-related gene 201 isolog T28M21.14 from *A. thaliana* BAC
AC002392_AT (SEQ ID NO: 69)	g3176709	putative anthranilate N-hydroxycinnamoyl/benzoyltransferase
AL031369_AT (SEQ ID NO: 70)	g3482975	unknown; putative protein
Z84383_AT (SEQ ID NO: 73)	g2239083	hydroxycinnamoyl:benzoyl-CoA:anthranilate N-hydroxycinnamoyl:benzoyl transferase
Z97338_AT (SEQ ID NO: 74)	g2244896	unknown; similar to HSR201 protein *N. tabacum*
Z97338_AT (SEQ ID NO: 60)	g2244897	unknown; hypothetical protein
AL049607_AT (SEQ ID NO: 61)	g4584530	unknown; putative protein

AF043464_CB (SEQ ID NO: 66)	g3170250	acetyl CoA:benzylalcohol acetyl transferase
Z70521_CM (SEQ ID NO: 72)	g1843440	unknown; expressed during ripening of melon (*Cucumis melo* L.) fruits
AF053307_CR (SEQ ID NO: 68)	g4091808	deacetylvindoline 4-*O*-acetyl transferase
AC004512_DC (SEQ ID NO: 67)	g3335350	unknown; similar to gb/Z84386 anthranilate N-hydroxycinnamoyl/ benzoyltransferase from *Dianthus caryophyllus*
X95343_NT (SEQ ID NO: 71)	g1171577	unknown; hypersensitive reaction in tobacco

At page 23, line 16 through page 24, line 2:

To determine the identity of the putative taxadienol acetyl transacylase, TAX1, TAX2, and TAX6 were subcloned in-frame into the expression vector pCWori+ (Barnes, *Methods Enzymol.* **272**:3-14, 1996) and expressed in *E. coli* JM109 cells. The transformed bacteria were cultured and induced with isopropyl ~~∃~~-β-D-thiogalactoside (IPTG), and cell-free extracts were prepared and evaluated for taxadienol acetyl transacylase activity using the previously developed assay procedures (Walker et al., *Arch. Biochem. Biophys.* **364**:273-279, 1999). Clone TAX1 (corresponding directly to Probe 1) expressed high levels of taxadienol acetyl transacylase activity (20% conversion of substrate to product), as determined by radiochemical analysis; the product of this recombinant enzyme was confirmed as taxadienyl-5~~∀~~-α-yl acetate by gas chromatography-mass spectrometry (GC-MS) (**Figure 5**). Clone TAX2 did not express taxadienol acetyl transacylase activity and was inactive with the [^{3}H]taxadienol and acetyl CoA co-substrates. However, the clone TAX2 may encode an enzyme for a step later in the Taxol™ biosynthetic pathway (TAX2 has been shown to correspond to Probe 2). Neither of the recombinant proteins expressed from TAX1 or TAX2 was capable of acetylating the advanced Taxol™ precursor 10-deacetyl baccatin III to baccatin III. Thus, based on the demonstration of functionally expressed activity, and the resemblance of the recombinant enzyme in substrate

specificity and other physical and chemical properties to the native form, clone TAX1 was confirmed to encode the *Taxus* taxadienol acetyl transacylase.

At page 25, lines 11-22:

A newly designed isolation and purification method is described below for the preparation of homogeneous taxadien-5~~∀~~-α-ol acetyl transacylase from *Taxus canadensis*. The purified protein was N-terminally blocked, thereby requiring internal amino acid microsequencing of fragments generated by proteolytic digestion. Peptide fragments so generated were purified by HPLC and sequenced, and one suitable sequence was used to design a set of degenerate PCR primers. Several primer combinations were employed to amplify a series of twelve related, gene-specific DNA sequences (Probes 1-12). Nine of these gene-specific sequences were used as hybridization probes to screen an induced *Taxus cuspidata* cell cDNA library. This strategy allowed for the successful isolation of eight full-length transacylase cDNA clones. The identity of one of these clones was confirmed by sequence matching to the peptide fragments described above and by heterologous functional expression of transacylase activity in *Escherichia coli*.

At page 26, lines 12-26:

Unfortunately, the previously described partial protein purification protocol, including an affinity chromatography step, did not yield pure protein for amino acid microsequencing, nor did the protocol yield protein in useful amounts, or provide a sufficiently simplified SDS-PAGE banding pattern to allow assignment of the transacetylase activity to a specific protein (Walker et al., *Arch. Biochem. Biophys.* **364:**273-279, 1999). Furthermore, numerous variations on the affinity chromatography step, as well as the earlier anion exchange and hydrophobic interaction chromatography steps, failed to improve the specific activity of the preparations due to the instability of the enzyme upon manipulation. Also, a five-fold increase in the scale of the preparation resulted in only marginally improved recovery (generally <5% total yield accompanied by removal of >99% of total starting protein). Furthermore, because the enzyme could not be purified to homogeneity, and attempts to improve stability by the addition of polyols (sucrose, glycerol), reducing agents ($Na_2S_2O_5$, ascorbate, dithiothreitol,

~~β~~ β-mercaptoethanol), and other proteins (albumin, casein) were also not productive (Walker et al., *Arch. Biochem. Biophys.* **364**:273-279, 1999), this approach had to be abandoned.

At page 27, lines 13-23:

The soluble enzyme fraction was subjected to ultrafiltration (DIAFLO™ YM 30 membrane, Millipore, Bedford, Massachusetts) to concentrate the fraction from 200 mL to 40 mL and to selectively remove proteins of molecular weight lower than the taxadien-5~~∀~~α-ol acetyl transacylase (previously established at 50,000 Da in Walker et al., *Arch. Biochem. Biophys.* **364**:273-279, 1999). Using a peristaltic pump, the concentrate (40 mL) was applied (2 mL/minute) to a column of *O*-diethylaminoethylcellulose (2.8 X 10 cm, Whatman DE-52, Fairfield, New Jersey) that had been equilibrated with "equilibration buffer" (30 mM HEPES buffer (pH 7.4) containing 3 mM DTT). After washing with 60 mL of equilibration buffer to remove unbound material, the proteins were eluted with a step gradient of the same buffer containing 50 mM (25 mL), 125 mM (50 mL), and 200 mM (50 mL) NaCl.

At page 27, lines 24-29:

The fractions were assayed as described previously (Walker et al., *Arch. Biochem. Biophys.* **364**:273-279, 1999), and those containing taxadien-5~~∀~~α-ol acetyl transacylase activity (125-mM and 200-mM fractions) were combined (100 mL, ~160 mM) and diluted to 5 mM NaCl (160 mL) by ultrafiltration (DIAFLO™ YM 30 membrane, Millipore, Bedford, Massachusetts) and repeated dilution with 30 mM HEPES buffer (pH 7.4) containing 3 mM DTT.

At page 29, lines 4-14:

The purified protein from multiple preparations as described above (>95% pure, ~100 pmol, 50 μg) was subjected to preparative SDS-PAGE (Laemmli, *Nature* **227**:680-685, 1970). The protein band at 50 kDa, corresponding to the taxadienol acetyl transacylase, was excised. Whereas treatment with V8 protease or treatment with cyanogen bromide (CNBr) failed to yield ~~sequencable~~ peptides suitable for sequencing, *in situ* proteolysis with endolysC (Caltech Sequence/Structure Analysis Facility, Pasadena, CA) and trypsin (Fernandez et al., *Anal. Biochem.* **218**:112-118, 1994) yielded a number of peptides, as determined by HPLC, and several

of these were separated, verified by mass spectrometry (Fernandez et al., *Electrophoresis* **19**:1036-1045, 1998), and subjected to Edman degradative sequencing, from which five distinct and unique amino acid sequences (designated SEQ ID NOs: 29-33) were obtained (**Figure 2**).

At page 29, line 18 through page 30, line 8:

A cDNA library was constructed from mRNA isolated from *T. cuspidata* suspension culture cells that had been induced to maximal Taxol™ production with methyl jasmonate for 16 hours. An optimized protocol for the isolation of total RNA from *T. cuspidata* cells was developed empirically using a buffer containing 100 mM Tri-HCl (pH 7.5), 4 M guanidine thiocyanate, 25 mM EDTA and 14 mM ~~β~~-β-mercaptoethanol. Cells (1.5 g) were disrupted at 0-4°C using a Polytron™ ultrasonicator (Kinematica AG, Switzerland; 4 X 15 second bursts at power setting 7), the resulting homogenate was adjusted to 2% (v/v) Triton X-100 and allowed to stand 15 minutes on ice. An equal volume of 3 M sodium acetate (pH 6.0) was then added, and the mixed solution was incubated on ice for an additional 15 minutes, followed by centrifugation at 15,000 *g* for 30 minutes at 4°C. The resulting supernatant was mixed with 0.8 volume of isopropanol and allowed to stand on ice for 5 minutes, followed by centrifugation at 15,000 *g* for 30 minutes at 4°C. The resulting pellet was dissolved in 8 mL of 20 mM Tris-HCl (pH 8.0) containing 1 mM EDTA, adjusted to pH 7.0 by addition of 2 mL of 2 M NaCl in 250 mM MOPS buffer (pH 7.0), and total RNA was recovered by passing this solution over a nucleic acid isolation column (Qiagen, Valencia, California) following the manufacturer's instructions. Poly(A)+ mRNA was then purified from total RNA by chromatography on oligo(dT) beads (Oligotex™ mRNA Kit, Qiagen), and this material was used to construct a library using the λZAPII™ cDNA synthesis kit and Gigapack™ III gold packaging kit from Stratagene, La Jolla, California, by following the manufacturer's instructions.

At page 32, lines 13-29:

The identification of TAX1 (SEQ ID NO: 27) and TAX2 (SEQ ID NO: 25) was accomplished using 1 μg of Probe 1 (SEQ ID NO: 1) that had been amplified by PCR, the resulting amplicon was gel-purified, randomly labeled with ~~[∀-[α-~~^{32}P]CTP (Feinberg and Vogelstein, *Anal. Biochem.* **137**:216-217, 1984), and used as a hybridization probe to screen membrane lifts of 5 X 10^5 plaques grown in *E. coli* XL1-Blue MRF'. Phage DNA was cross-

linked to the nylon membranes by autoclaving on fast cycle 3-4 minutes at 120°C. After cooling, the membranes were washed 5 minutes in 2 X SSC, then 5 minutes in 6 X SSC (containing 0.5% SDS, 5 X Denhardt's reagent, 0.5 g Ficoll (Type 400, Pharmacia, Piscataway, New Jersey), 0.5 g polyvinylpyrrolidone (PVP-10), and 0.5 g bovine serum albumin (Fraction V, Sigma, Saint Louis, Missouri) in 100 mL total volume). Hybridization was then performed for 20 hours at 68°C in 6 X SSC, 0.5% SDS and 5 X Denhardt's reagent. The nylon membranes were then washed two times for 5 minutes in 2 X SSC with 0.1% SDS at 25°C, and then washed 2 X 30 minutes with 1 X SSC and 0.1% SDS at 68°C. After washing, the membranes were exposed for 17 hours to Kodak (Rochester, New York) XAR film at -70°C (Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, cold Spring Harbor Laboratory Press, cold Spring Harbor, NY, 1989).

At page 34, lines 11-20:

Isolated transformants for each full-length insert are grown to A_{600} = 0.5 at 37°C in 50 mL Luria-Bertani medium supplemented with 50 µg ampicillin/mL, and a 1-mL inoculum added to a large scale (100 mL) culture of Terrific Broth (6 g bacto-tryptone, DIFCO Laboratories, Spark, Maryland, 12 g yeast extract, EM Science, Cherryhill, New Jersey, and 2 mL glycerol in 500 mL water) containing 50 µg ampicillin/mL and thiamine HCl (320 mM) and grown at 28°C for 24 hours. Approximately 24 hours after induction with 1 mM isopropyl ~~∃~~-β-D-thiogalactoside (IPTG), the bacterial cells are harvested by centrifugation, disrupted by sonication in assay buffer consisting of 30 mM potassium phosphate (pH 7.4), or 25 mM MOPSO (pH 7.4), followed by centrifugation to yield a soluble enzyme preparation that can be assayed for transacylase activity.

At page 34, line 24-31:

A specific assay for acetyl CoA:taxa-4(20),11(12)-dien-5~~∀~~-α-ol *O*-acetyl transacylase has been described previously (Walker et al., *Arch. Biochem. Biophys*. **364**:273-279, 1999, herein incorporated by reference). Generally the assay for taxoid ~~acyltransacylases~~ acyltransferases involves the CoA-dependent acyl transfer from acetyl CoA (or other acyl or aroyl CoA ester) to a taxane alcohol, and the isolation and chromatographic separation of the

product ester for confirmation of structure by GC-MS (or HPLC-MS) analysis. For another example of such an assay, see Menhard and Zenk, *Phytochemistry* **50**:763-774, 1999.

In the Abstract:

At page 57, lines 2-4:

Transacylase enzymes and the use of such enzymes to produce Taxol™, related taxoids, as well as intermediates in the Taxol™ biosynthetic pathway are disclosed. Also disclosed are nucleic acid sequences encoding the transacylase enzymes. Specific non-limiting embodiments include nucleic acid sequences encoding 10-deacetylbaccatin III-10-O-acetyl transferase.

In the Claims:

1. (Cancelled) ~~A purified protein, comprising an amino acid sequence selected from the group consisting of: SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 45, 50, 52, 54, 56, and 58~~.

3. (Amended). An isolated nucleic acid molecule ~~encoding a protein according to claim 1~~comprising a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO: 45.

4. (Amended). ~~An~~ The isolated nucleic acid molecule according to claim 3, ~~further comprising a~~ wherein the nucleic acid sequence ~~selected from the group consisting of:~~comprises the nucleic acid sequence shown in SEQ ID NOs: ~~1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 44, 49, 51, 53, 55, and 57~~.

5. (Original). A recombinant nucleic acid molecule, comprising a promoter sequence operably linked to a nucleic acid molecule according to claim 3.

6. (Original). A cell transformed with a recombinant nucleic acid molecule according to claim 5.

8. (Amended). An isolated nucleic acid molecule that:

(a) hybridizes under ~~low~~ very high stringency conditions with a nucleic acid ~~probe, the probe comprising a~~ sequence ~~selected from the group consisting of~~ as set forth in SEQ ID NOs: ~~1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27,~~ 44, ~~49, 51, 53, 55, and 57 and fragments thereof~~; and

(b) encodes a protein having transacylase activity, wherein the protein uses as a substrate a taxoid with a 10-hydroxyl group.

9. (Cancelled) ~~A transacylase encoded by the nucleic acid molecule of claim 8~~.

10. (Original). A recombinant nucleic acid molecule, comprising a promoter sequence operably linked to a nucleic acid molecule according to claim 8.

11. (Original). A cell transformed with a recombinant nucleic acid molecule according to claim 10.

14. (Amended). An isolated nucleic acid molecule that:

(a) has at least ~~60~~90% sequence identity with a nucleic acid sequence ~~selected from the group consisting of~~ as set forth in SEQ ID NOs: ~~1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27,~~ 44, ~~49, 51, 53, 55, and 57~~; and

(b) encodes a protein having transacylase activity, wherein the protein uses as a substrate a taxoid with a 10-hydroxyl group.

16. (Cancelled) ~~A nucleic acid molecule identified by the method of claim 15~~.

18. (Cancelled) ~~A transacylase encoded by the nucleic acid molecule of claim 16~~.

23. (Cancelled) ~~A purified protein having transacylase activity, comprising an amino acid sequence selected from the group consisting of:~~

~~(a) an amino acid sequence selected from the group consisting of SEQ ID NOs: 26, 28, 50, 52, 54, 56, and 58;~~

~~(b) an amino acid sequence that differs from the amino acid sequence specified in (a) by one or more conservative amino acid substitutions; and~~

~~(c) an amino acid sequence having at least 60% sequence identity to the sequences specified in (a) or (b).~~

24. (Amended). An isolated nucleic acid molecule encoding a protein comprising an amino acid sequence ~~according to claim 23~~selected from the group consisting of.

(a) an amino acid sequence that differs from SEQ ID NO: 45 by one or more conservative amino acid substitutions; and

(b) an amino acid sequence having at least 90% sequence identity to the sequences specified in (a).

wherein the protein has transacylase activity and uses as a substrate a taxoid with a 10-hydroxyl group.

25. (Cancelled)~~An isolated nucleic acid molecule according to claim 24, further comprising a sequence selected from the group consisting of SEQ ID NOs: 25, 27, 49, 51, 53, 55, and 57~~.

26. (Original). A recombinant nucleic acid molecule, comprising a promoter sequence operably linked to the nucleic acid molecule of claim 24.

27. (Original). A cell transformed with a recombinant nucleic acid molecule according to claim 26.

FROM PEPTIDE FRAGMENT SEQUENCE 2

NH2-	I	L	V	Y	Y	P	P	-COOH	(Residues 1-7 of SEQ ID NO: 30)
5′	ATI	CTI	GTI	TAT	TAT	CCI	CC	3′	AT-FOR1 (SEQ ID NO: 34)
		T	C	C	C	C			
			A			A			

NH2-	Y	Y	P	P	F	A	G	-COOH	(Residues 4-10 of SEQ ID NO: 30)
5′	TAT	TAT	CCI	CCI	TTT	GCI	GG	3′	AT-FOR2 (SEQ ID NO: 35)
	C	C	C	C	C	C			
			A	A		A			

FROM SEQUENCE HOMOLOGY CONSIDERATIONS

NH2-	F	Y	P	F	A	G	R	-COOH	(SEQ ID NO: 39)
5′	TTC	TAT	CCI	TTC	GCI	GGI	AG	3′	AT-FOR3 (SEQ ID NO: 36)
	T	C		T	C	C			
					A	A			

NH2-	Y	Y	P	L	A	G	R	-COOH	(SEQ ID NO: 40)
5′	TAC	TAT	CCI	TTI	GCI	GGI	AG	3′	AT-FOR4 (SEQ ID NO: 37)
	T	C		C	C	C	C		
					A	A			

NH2-	D	F	G	W	G	K	P	-COOH	(SEQ ID NO: 41)
3′	CTA	AAA	CCI	ACC	CCI	TTT	GG	5′	AT-REV1 (SEQ ID NO: 38)
	G	G	C		C	C			
			A		A				

FIG. 4

TAX1 (SEQ ID NO: 28)		0
TAX2 (SEQ ID NO: 26)		0
aab61522 (SEQ ID NO: ~~61~~ 59)		0
aab61523 (SEQ ID NO: 62)		0
aab95283 (SEQ ID NO: 63)		0
aab97723 (SEQ ID NO: 64)		0
aac17079 (SEQ ID NO: 65)	MAAVSVASAELPPPPQDGETLSNVPQTLSGEDCKKQRIQRPKSKNAEKCT	50
aac18062 (SEQ ID NO: 66)		0
aac27152 (SEQ ID NO: 67)		0
aac99311 (SEQ ID NO: 68)		0
aad12025 (SEQ ID NO: 69)		0
caa20531 (SEQ ID NO: 70)		0
caa64636 (SEQ ID NO: 71)		0
caa94432 (SEQ ID NO: 72)		0
cab06427 (SEQ ID NO: 73)		0
cab10318 (SEQ ID NO: 74)		0
cab10319 (SEQ ID NO: ~~75~~ 60)		0
cab40761 (SEQ ID NO: ~~76~~ 61)		0

8

FIG. 6A

TAX1 (SEQ ID NO: 28)	. . . . .	0
TAX2 (SEQ ID NO: 26)	. . . . .	0
aab61522 (SEQ ID NO: ~~61~~ 59)	. . . . .	0
aab61523 (SEQ ID NO: 62)	. . . . .	0
aab95283 (SEQ ID NO: 63)	. . . . .	0
8 aab97723 (SEQ ID NO: 64)	. . . . .	0
aac17079 (SEQ ID NO: 65)	V K C V N T C I R S G D G E G P I N I R R F Q R I A W Q I E G I Q V T V S C F F V T C G K T R S S S	100
aac18062 (SEQ ID NO: 66)	. . . . .	0
aac27152 (SEQ ID NO: 67)	. . . . .	0
aac99311 (SEQ ID NO: 68)	. . . . .	0
aad12025 (SEQ ID NO: 69)	. . . . .	0
caa20531 (SEQ ID NO: 70)	. . . . .	0
caa64636 (SEQ ID NO: 71)	. . . . .	0
caa94432 (SEQ ID NO: 72)	. . . . .	0
cab06427 (SEQ ID NO: 73)	. . . . .	0
cab10318 (SEQ ID NO: 74)	. . . . .	0
cab10319 (SEQ ID NO: ~~76~~ 60)	. . . . .	0
cab40761 (SEQ ID NO: ~~76~~ 61)	. . . . .	0

FIG. 6B

```
TAX1 (SEQ ID NO: 28) . . . . . MEKTDLHVNLIEKVMVGPSPPL . . . . . P  23
TAX2 (SEQ ID NO: 26) . . . . . MGRFNVDMIERVIVAPCLQS . . . . . P  21
aab61522 (SEQ ID NO: ~~64)~~ 59 . . . . . 0
aab61523 (SEQ ID NO: 62) . . . . . MEKNVEILSREIVKPSSPTP . . . DD  22
aab95283 (SEQ ID NO: 63) . . . . . MPSLEKSVTIISRNRVFPDQKST . . . LV  25
aab97723 (SEQ ID NO: 64) . . . . . MASCIQELHFTHLHIPVTINQQFLVHPSSPTPANQSP  37
aac17079 (SEQ ID NO: 65) NNPHHTTFFILSENNNQMGEAAEQARGFHVTTTRKQVITAALPLQ . . . DH  147
aac18062 (SEQ ID NO: 66) . . . . . MNVTMHSKKLLKPSIPTP . . . NH  20
aac27152 (SEQ ID NO: 67) . . . . . MGSSYQESPPLLLEDLKVTIKESTLIFPSEET . . . . SE  34
aac99311 (SEQ ID NO: 68) . . . . . MESGKISVETETLSKTLIKPSSPTP . . . QS  27
aad12025 (SEQ ID NO: 69) . . . . . MAPITFRKSYTIVPAEPT . . . . WS  20
caa20531 (SEQ ID NO: 70) . . . . . MANQRKPILPLLLEKKPVELVKPSKHTHC . . . .  29
caa64636 (SEQ ID NO: 71) . . . . . MDSKQSSELVFTVRRQKPELIAPAKPT . . . . . P  28
caa94432 (SEQ ID NO: 72) . . . . . DFSFHVRKCQPELIAPANPT . . . . . P  21
cab06427 (SEQ ID NO: 73) . . . . . MSIQIKQSTMVRPAEET . . . . PN  19
cab10318 (SEQ ID NO: ~~74)~~ 60 . . . . . METMTMKVETISKEIIKPSSPTP . . . NN  25
cab10319 (SEQ ID NO: ~~75)~~ 61 . . . . . MEAKLEVTGKEVIKPASPSP . . . RD  22

cab40761 (SEQ ID NO: 76) . . . . . MPMLMATRIDIIQKLNVYPRFQN  23
```

FIG. 6C

```
TAX1 (SEQ ID NO: 28) KTTLQLSSIDNLPGVRGSIFNALLIYNASPSPTMISADP.......AKPI  66
TAX2 (SEQ ID NO: 26) KNILHLSPIDNKT...RGLTNILSVYNASQRVS.VSADP.......AKTI  60
aab61522 (SEQ ID NO: 61) 59. .....                                        0
aab61523 (SEQ ID NO: 62) KRILNLSLLDILSSPMYTGALLFYAADPQNLLGFSTEET.......SLKL  65
aab95283 (SEQ ID NO: 63) DLKLSVSDLPMLSCHYIQKGCLFTCPN......LPLPAL.......ISHL  62
aab97723 (SEQ ID NO: 64) HHSLYLSNLDDIIGARVFTPSVYFYPSTNNRESFV..........LKRL  76
aac17079 (SEQ ID NO: 65) W..LPLSNLDLLLPPLNVHVCFCYKKP....LHFTNTVA.......YETL  184
aac18062 (SEQ ID NO: 66) LQKLNLSLLDQIQIPFYVGLIFHY.....ETLSDNSDIT.......LSKL  58
aac27152 (SEQ ID NO: 67) RKSMFLSNVDQILN...FDVQTVHFFRPNKEFPPEMV.........SEKL  72
aac99311 (SEQ ID NO: 68) LSRYNLSYNDQNIYQTCVSVGFFYENPDGIEISTIRE..........QL  66
aad12025 (SEQ ID NO: 69) .GRFPLAEWDQV..GTITHIPTLYFYDKPSESFQGNV.........VEIL  58
caa20531 (SEQ ID NO: 70) .ETLSLSTLDNDPFNEVMYATIYVFKANGKNLD....DP.......VSLL  67
caa64636 (SEQ ID NO: 71) RETKFLSDIDDQEGLR...FQIPVIQFYHKDSSMGRKDP.......VKVI  68
caa94432 (SEQ ID NO: 72) YEFKQLSDVDDQQSLR...LQLPFVNIYPHNPSLEGRDP.......VKVI  61
cab06427 (SEQ ID NO: 73) .KSLWLSNIDMILRTPYSHTGAVLIYKQPDNN.EDNIHPSSSMYFDANIL  67
cab10318 (SEQ ID NO: 74) LQTLQLSIYDHILPPVYTVAFLFYTKNDL....ISQEHT.......SHKL  64
cab10319 (SEQ ID NO: 75) R..LQLSILDLYCPGIYVSTIFFY.....DLITESSEVF.......SENL  58
cab40761 (SEQ ID NO: 76) HDKKKLITLSNLDRQCPLLMYSVFFYKNTTTRDFDSV.........FSNL  64
```

60 61

FIG. 6D

```
TAX1 (SEQ ID NO: 28) REALAKILVVYYPPFAGRL.RETENGDLEVECTGE.GAMFLEAMADNELSV 114
TAX2 (SEQ ID NO: 26) REALSKVLVVYYPPFAGRL.RNTENGDLEVECTGE.GAVFVEAMADNDLSV 108
aab61522 (SEQ ID NO: 61) ...............................................MSQ 3
aab61523 (SEQ ID NO: 62) KKSLSKTLPIFYPLAGRII.GS.....FVECNDEGAVFIEARVDH.LLSE 108
aab95283 (SEQ ID NO: 63) KHSLSITLTHFPPLAGRLS.TSSSGHVFLTCNDAGADFVFAQAKSIHVSD 111
aab97723 (SEQ ID NO: 64) QDALSEVLVPYYPLSGRL.REVENGKLEVFFGEEQGVLMVSANSSMDLAD 125
aac17079 (SEQ ID NO: 65) KTALAETLVSYYAFAGELV.TNPTGEPEILCNNRGVDFVEAGAD.VELRE 232
aac18062 (SEQ ID NO: 66) ESSLSETLTLYYHVAGRYN.GT...DCVIECNDQGIGYVETAFD.VELHQ 103
aac27152 (SEQ ID NO: 67) RKALVKLMDAYEFLAGRLRVDPSSGRLDVDCNGA.GAGFVTAASDYTLEE 121
aac99311 (SEQ ID NO: 68) QNSLSKTLVSYYPFAGKVV.KN...DY.IHCNDDGIEFVEVRI.RCRMND 110
aad12025 (SEQ ID NO: 69) KTSLSRVLVHFYPMAGRLRWLP.RGRFELNCNAE.GVEFIEAESEGKLSD 106
caa20531 (SEQ ID NO: 70) RKALSELLVHYYPLSGKLMRSESNGKLQLVYLGE.GVPFEVATSTLDLSS 116
caa64636 (SEQ ID NO: 71) KKAIAETLVFYYPFAGRL.REGNGRKLMVDCTGE.GIMFVEADADVTLEQ 116
caa94432 (SEQ ID NO: 72) KEAIGKALVFYYPLAGRL.REGPGRKLFVECTGE.GILFIEADADVSLEE 109
cab06427 (SEQ ID NO: 73) IEALSKALVPFYPMAGRLK.IN.GDRYEIDCNAE.GALFVEAESSHVLED 114
cab10318 (SEQ ID NO: 74) KTSLSETLTKFYPLAGRIT.GV.....TVDCTDEGAIFVDARVNNCPLTE 108
cab10319 (SEQ ID NO: 75) KLSLSETLSRFYPLAGRIE.GL.....SISCNDEGAVFTEARTDL.LLPD 101
cab40761 (SEQ ID NO: 76) KLGLEETMSVWYPAAGRLGLDGGGCKLNIRCNDGGAVMVEAVATGVKLSE 114
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FIG. 6E

59

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TAX1 (SEQ ID NO: 28)      LGD.FDDSNPSFQ.QLLFSLPLDTNF.....KDLSLLVVQVTREFTCG.GF 156
TAX2 (SEQ ID NO: 26)      LQD.FNEYDPSFQ.QLVFNLREDVNI.....EDLHLLTVQVTREFTCG.GF 150
aab61522 (SEQ ID NO: 61)  ILEN.PNPN.ELNKLHPFEFHEVSDVP.........LTVQLTFFECG.GL  41
aab61523 (SEQ ID NO: 62)  FLKC.PVPE.SLELLIP...VEAKSRE...AVTWEVLLIQANFFSCG.GL 149
aab95293 (SEQ ID NO: 63)  VIAGIDVPD.VVKEFFTYDR..AVSYE...GHNRPILAVQVTELN..DGV 153
aab97723 (SEQ ID NO: 64)  LGDLTVPNPAWLPLIFRNPGEEAYKI.....LEMPLLIAQVTFFTCG.GF 169
aac17079 (SEQ ID NO: 65)  LNLY.DPDE.SIAKLVPIKKHG.............VIAIQVTQLKCG.SI 266
aac18062 (SEQ ID NO: 66)  FLLG.EESN.NLDLLVGL...SGFLSE...TETPPLAAIQLNMFKCG.GL 144
aac27152 (SEQ ID NO: 67)  LGD.LVYPNPAFAQLVTSQLQ.SLPKD.....DQPLFVFQITSFKCG.GF 163
aac99311 (SEQ ID NO: 68)  ILKY.ELRS.YARDLVLPKRVTVGSED...TTA....IVQLSHFDCG.GL 150
aad12025 (SEQ ID NO: 69)  FKD.FS.PTPEFENLM.PQVNYKNPIE.....TIPLFLAQVTKFKCG.GI 147
caa20531 (SEQ ID NO: 70)  LN.....YIENLDDQVALRLVPEIEIDYESNVCYHPLALQVTKFACG.GF 160
caa64636 (SEQ ID NO: 71)  FGDELQPPFPCLE.ELLYDVPDSAGV.....LNCPLLLIQVTRLRCG.GF 159
caa94432 (SEQ ID NO: 72)  FWDTLPYSLSSMQNNIIHNALNSDEV.....LNSPLLLIQVTRLKCG.GF 153
cab06427 (SEQ ID NO: 73)  FGD.FR.PNDELHRVMVPTCDYSKGIS.....SFPLLMVQLTRFRCG.GV 156
cab10318 (SEQ ID NO: 74)  FLKC.PDFD.ALQQLLPLDVVDNPYVA...AATWPLLLVKATYFGCG.GM 152
cab10319 (SEQ ID NO: 75)  FLRN.LNTD.SLSGFLPTLAAGE...S...PAAWPLLSVKVTFFGSGSGV 143
cab40761 (SEQ ID NO: 76)  LGDLTQYNEFYENLVYKPSLDGDFSV.......MPLVVAQVTRFACG.GY 156
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FIG. 6F

TAX1 (SEQ ID NO: 28)	VVGVSFHHGVCDGRGAAQFLKGLAEMAR.GEVKLS..........LEPIW	195
TAX2 (SEQ ID NO: 26)	VVGTRFHHSVSDGKGIGQLLKGMGEMAR.GEFKPS..........LEPIW	189
aab61522 (SEQ ID NO: 61)	ALGIGLSHKLCDALSGLIFVNSWAAFARGQTDE..........IITPSF	80
aab61523 (SEQ ID NO: 62)	VITICVSHKITDATSLAMFIRGWAESSRG...L.........GITLIPSF	187
aab95283 (SEQ ID NO: 63)	FIGCSVNHAVTDGTSLWNFINTFAEVSRGAKNVT.....RQPDFTRESVL	198
aab97723 (SEQ ID NO: 64)	SLGIRLCHCICDGFGAMQFLGSWAATAKTGKLIAD..........PEPVW	209
aac17079 (SEQ ID NO: 65)	VVGCTFDHRVADAYSMNMFLLSWAEISRSDVPI.........SCV..PSF	305
aac18062 (SEQ ID NO: 66)	VIGAQFNHIIGDMFTMSTFMNSWAKACRVGIKE...........VAHPTF	183
aac27152 (SEQ ID NO: 67)	AMGISTNHTTFDGLSFKTFLENLASLLH..EKPLS..........TPPCN	201
aac99311 (SEQ ID NO: 68)	AVAFGISHKVADGGTIASFMKDWAASACYLSSS.........HHVPTPLL	191
aad12025 (SEQ ID NO: 69)	SLSVNVSHAIVDGQSALHLISEWGRLAR..GEPLE..........TVPFL	185
caa20531 (SEQ ID NO: 70)	TIGTALTHAVCDGYGVAQIIHALTELA.AGKTEPS..........VKSVW	199
caa64636 (SEQ ID NO: 71)	IFALRLNHTMSDAPGLVQFMTAVGEMAR.GGSAPS..........ILPVW	198
caa94432 (SEQ ID NO: 72)	IFGLCFNHTMADGFGIVQFMKATAEIAR.GAFAPS..........ILPVW	192
cab06427 (SEQ ID NO: 73)	SIGFAQHHHVCDGMAHFEFNNSWARIAK..GLLPA..........LEPVH	194
cab10318 (SEQ ID NO: 74)	AIGICITHKIADAASISTFIRSWAATARGENDA.........AAMESPVF	193
cab10319 (SEQ ID NO: 75)	AVSVSVSHKICDIASLVTFVKDWATTTAKGKSN.........STIE...F	181
cab40761 (SEQ ID NO: 76)	SIGIGTSHSLFDGISAYEFIHAWASNSHIHNKSNSKITNKKEDVVIKPVH	206

FIG. 6G

TAX1 (SEQ ID NO: 28)	NRELVKLD...DP..KYLQFFHF..EFLRAP......SIV.....EKIVQ	227
TAX2 (SEQ ID NO: 26)	NREMVKPE...DI..MYLQFDHF..DFIHPP......LNL.....EKSIQ	221
aab61522 (SEQ ID NO: 61)	DLAKMFPPCDIEN..........LNMATGITKE.....NIVT........	107
aab61523 (SEQ ID NO: 62)	TASEVFPKPLDEL..........PSKPMDRKEEVEEMS.CVT........	218
aab95283 (SEQ ID NO: 63)	ISPAVLKVPQGGPKVTFDENAPLRERIFSFSRESIQELKAVVNKK.....	243
aab97723 (SEQ ID NO: 64)	DRETFKPR...NP..PMVKYPHH..EYLPIEERSNLTNSLWD...TKPLQ	249
aac17079 (SEQ ID NO: 65)	RRSLLNPRRPLVMDPSIDQIYMPVTSLPPPQETTNPENLLAS........	347
aac18062 (SEQ ID NO: 66)	GLAPLMPSAKVLN..........IPPPPSFEG.....VKFVS........	210
aac27152 (SEQ ID NO: 67)	DRTLLKARDPPS.....VAFPHH..EL..VKFQDCETTTVFEATSEHLDF	242
aac99311 (SEQ ID NO: 68)	VSDSIFPRQDNII..........CEQFPTSK.......NCVE........	216
aad12025 (SEQ ID NO: 69)	DRKILWAGEPLPPFVSPPKFDHK..EFDQPPFLIGETDNVEERKKKTIV.	232
caa20531 (SEQ ID NO: 70)	QRERLVGKIDNKP..GKVPGSHI..D.....GFLATSAYLPT...TDVVT	237
caa64636 (SEQ ID NO: 71)	CRELLNAR...NP..PQVTCTHH..EYDEVRDTKGTIIPL.....DDMVH	236
caa94432 (SEQ ID NO: 72)	QRALLTAR...DP..PRITFRHY..EYDQVVDMKSGLIPV.....NSKID	230
cab06427 (SEQ ID NO: 73)	DRYLHLRPRNPPQI....KYSHS..QFE..PFVPSLPNELLDGKTNKSQ.	235
cab10318 (SEQ ID NO: 74)	AGANFYPPANEAF.............KLPADEQAGKRS.SIT........	221
cab10319 (SEQ ID NO: 75)	AETTIYPPPPSHM..........YEQFPSTDSDSNITSKYVL........	213
cab40761 (SEQ ID NO: 76)	DRRNLLVNRDAVRETNAAAICHLYQLIKQAMMTYQEQNRNLELPDSGFVI	256

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FIG. 6H

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TAX1 (SEQ ID NO: 28) TYFIIDFETINYIKQSV.MEEC.....KEF 251
TAX2 (SEQ ID NO: 26) ASMVISFERINYIKRCM.MEEC.....KEF 245
aab61522 (SEQ ID NO: 64) RRFVFLRSSVESLRERFSGNK.....KIR.AT 133
aab61523 (SEQ ID NO: 62) KRFVFDASKIKKLRAK.ASRN.....LVKNPT 244
aab95283 (SEQ ID NO: 63) KWLTVDNGEIDGVELLGKQSNDKLNGKENGILTEMLESLFGRNDAVSKPV 293
aab97723 (SEQ ID NO: 64) KCYRISKEFQCRVKSIA.QGED.....PTL 273
aac17079 (SEQ ID NO: 65) RIYYIKANALQELQTLASSSKN.....GKRT 373
aac18062 (SEQ ID NO: 66) KRFVFNENAITRLRKEATEEDGDGDD.....DQKKKRPS 244
aac27152 (SEQ ID NO: 67) KIFKLSSEQIKKLKERA..SET.....SNG 265
aac99311 (SEQ ID NO: 68) KTFIFPPEAIEKLKSKAVEFG.....IEKPT 242
aad12025 (SEQ ID NO: 69) VMLPLSTSQLQKLRSKANGSKH.....SDP 257
caa20531 (SEQ ID NO: 70) ETINIRAGDIKRLKDSM.MKEC.....EYL 261
caa64636 (SEQ ID NO: 71) KSFFFGPSEVSALRRFV.PHHL.....RK. 259
caa94432 (SEQ ID NO: 72) QLFFFSQLQISTLRQTL.PAHL.....HD. 253
cab06427 (SEQ ID NO: 73) TLFILSREQINTLKQKLDLSNN.....TTR 260
cab10318 (SEQ ID NO: 74) KRFVFEASKVEDLRTKAASEE.....TVDQPT 248
cab10319 (SEQ ID NO: 75) KRFVFEPSKIAELKHKAASES.....VPVPT 239
cab40761 (SEQ ID NO: 76) KTFELNGDAIESMKKKSLEG..... 276
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FIG. 6I

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TAX1 (SEQ ID NO: 28) .CS..SFEVASAMTWIARTRAFQIPESEY.......VKILFGMDMRNSFN 291
TAX2 (SEQ ID NO: 26) .FS..AFEVVVALIWLARTKSFRIPPNEY.......VKIIFPIDMRNSFD 285
aab61522 (SEQ ID NO: 64) RVE.....VLSVFIWSRF..MASTNHDDKTGKIYT...LIHPYNLRRQAD 173
aab61523 (SEQ ID NO: 62) RVE.....AVTALFWRCV..TKVSRLSSLTPRTSV...LQILYNLRGKVD 284
aab95283 (SEQ ID NO: 63) AVEISSFQSLCALLWRAITRARKLPSSKTTT.......FRMAYNCRHRLS 336
aab97723 (SEQ ID NO: 64) VCS..TFDAMAAHIWRSWVKALDVKPLDYN......LRLTFSYNVRTRLE 315
aac17079 (SEQ ID NO: 65) KLE.....SFSAFLWKLVAEHAAKDPVPIKTSK.....LGIVYDGRRRLM 413
aac18062 (SEQ ID NO: 66) RVD.....LVTAFLSKSLIEMDCAKKEQTKSRPSL...MVHMMNLRKRTK 286
aac27152 (SEQ ID NO: 67) NVRVTGFNVVTALVWRCKALSVAAEEGEET.NLERESTILYAYDIRGRL. 313
aac99311 (SEQ ID NO: 68) RVE.....VLTAFLSRCATVAGKSAAKNNNCGQSLPFPVLQAINLRPILE 287
aad12025 (SEQ ID NO: 69) AKGFTRYETVTGHVWRCACKARGHSPEQPT.AL.......GICIDTRSRM. 299
caa20531 (SEQ ID NO: 70) KESFTTYEVLSSYIWKLRSRALKLNPDGIT.......V.LGVAYGIRHVLD 304
caa64636 (SEQ ID NO: 71) .CS..TFELLTAVLWRCRTMSLKPDPEEE.......VRALCIYNARSRFN 299
caa94432 (SEQ ID NO: 72) .CP..SFEVLTAYVWRLRTIALQFKPEEE.......VRFLCVMNLRSKID 293
cab06427 (SEQ ID NO: 73) ...LSTYEVVAAHVWRSVSKARGLSDHEEI.KL.......IMPYDGRSRIN 300
cab10318 (SEQ ID NO: 74) RVE.....SVTALIWKCF..VASSK..TTTCDHKV...LVQLANLRSKIP 286
cab10319 (SEQ ID NO: 75) RVE.....AIMSLIWRCA..RNSSRSNLLIPRQAV...MWQAMDIRLRIP 279
cab40761 (SEQ ID NO: 76) .FMCSSFEFLAAHLWKARTRALGLRRDA.......MVCLQFAVDIRKRTE 318
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FIG. 6J

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TAX1 (SEQ ID NO: 28) P . P L P S G Y Y G N S I G T A C A V D N V Q D . . L L S G . S L L R A I M I I K K S K V S L . . .  334
TAX2 (SEQ ID NO: 26) S . P L P K G Y Y G N A I G N A C A M D N V K D . . L L N G . S L L Y A L M L I K K S K F A L . . .  328
aab61522 (SEQ ID NO: 61) P . D I P D N M F G N I M R F S V T V P M M I I N . . E N D E E K A S L V D Q M R E E I R K I . . .  217
aab61523 (SEQ ID NO: 62) S . . L C E N T I G N . M L S L M I . . L K N E E . . A A I E R I Q D V V D E I R R A K E I F . . .  324
aab95283 (SEQ ID NO: 63) P . K L N P E Y F G N A I . . . . . . . . . . . . . Q S V P T F A T A A E V L S R D L K W C . . .  368
aab97723 (SEQ ID NO: 64) T L K L R K G F Y G N V V C L A C A M S S V E S . . L I N D . S L S K T T R L V Q D A R L R V . . .  359
aac17079 (SEQ ID NO: 65) E . K E N N T Y F G N V L S V P F G G Q R I D D L I S K P L S W V T E E V H R F L K K . . . . . . .  455
aac18062 (SEQ ID NO: 66) L . A L E N D V S G N F F . . . . . . I V V N A . . E S K I T V A P K I T D L T E S L G S A . . .  323
aac27152 (SEQ ID NO: 67) N P E L P P S Y T G N A V L T A Y A K E K C K A . . L L E E . P F G R I V E M V G E G S K R I . . .  357
aac99311 (SEQ ID NO: 68) . . . L P Q N S V G N L V S I Y F S R T I K E N D Y L N E K E Y T K L V I N E L R K E K Q K I . . .  331
aad12025 (SEQ ID NO: 69) E P P L P R G Y F G N A T L D V V A A S T S G E . . L I S N . E L G F A A S L I S K A I K N V . . .  343
caa20531 (SEQ ID NO: 70) P . P L P K G Y Y G N A Y I D V Y V E L T V R E . . L E E S . S I S N I A N R V K K A K K T A Y E K  350
caa64636 (SEQ ID NO: 71) P . P L P T G Y Y G N A F A F P V A V L T A A K . . L S K N . P L G Y A L E L V K K T K S D V . . .  342
caa94432 (SEQ ID NO: 72) I . P L . . G Y Y G N A V V V P A V I T T A A K . . L C G N . P L G Y A V D L I R K A K A K A . . .  334
cab06427 (SEQ ID NO: 73) N P S L P K G Y C G N V V F L A V C T A T V G D . . L S C N . P L T D T A G K V Q E A L K G L . . .  344
cab10318 (SEQ ID NO: 74) S . L L Q E S S I G N L M F S S V V . . L S I G R . . G G E V K I E E A V R D L R K K K E E L . . .  328
cab10319 (SEQ ID NO: 75) S . S V A P K D V I G N L Q S G F S . . L K K D A . . E S E F E I P E I V A T F R K N K E R V . . .  321
cab40761 (SEQ ID NO: 76) T . P L P E G F S G N A Y V L A S V A S T A R E . . L L E E L T L E S I V N K I R E A K K S I . . .  362
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FIG. 6K

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TAX1 (SEQ ID NO: 28) . . NDNF . KSRAVVKPSELDVN . . . . . MNHENVVAFADWSRL 367
TAX2 (SEQ ID NO: 26) . . NENF . KSRILTKPSTLDAN . . . . . MKHENVVGCGDWRNL 361
aab61522 (SEQ ID NO: 61) . . DAVYVKKLQEDNRGHL . . . . . EFLNKQASGFVNGEIVSFSFTSLCKF 259
aab61523 (SEQ ID NO: 62) . . S . . . LNCKEMSKSSSRIFELLEEIG . KVYGRG . . NEMDLWMSNSWCKL 366
aab95283 (SEQ ID NO: 63) . . ADQLNQSVAAHQDGRIRSVVADWEANPRCFPLGNADGASVTMGSSPRF 416
aab97723 (SEQ ID NO: 64) . . SEDYLRSMVDYVDVKRPKR . . . . . LEFGGKLTITQWTRF 393
aac17079 (SEQ ID NO: 65) . . . . . SVTKEHFLNLIDWVETCRPTPAVSRIYSVGSDDGPAFVVSSGRSF 500
aac18062 (SEQ ID NO: 66) . . CGEIISEVAKVDDAEVVSSMVLNSVREFYYEWGKGEKNVFLYTSWCRF 371
aac27152 (SEQ ID NO: 67) . . TDEYARSAIDWGELYKG . . . . . FPHGEVLVSSWWKL 388
aac99311 (SEQ ID NO: 68) . . KNLSREKLTYVAQMEEFVKSLKEFDISNFL . . . . . DIDAYLSDSWCRF 374
aad12025 (SEQ ID NO: 69) . . TNEYVMIGIEYLKNQKDLKKFQDLHALGSTEGPFYGNPNLGVVSWLTL 391
caa20531 (SEQ ID NO: 70) GYIEEELKNTERLMRDDSMFE . . . . . GVSDGLFFLTDWRNI 386
caa64636 (SEQ ID NO: 71) . . TEEYMKSVADLMVLKGRPH . . . . . FTVVRTFLVSDVTRG 376
caa94432 (SEQ ID NO: 72) . . TMEYIKSTVDLMVIKGRPY . . . . . FTVVGSFMMSDLTRI 368
cab06427 (SEQ ID NO: 73) . . DDDYLRSAIDHTESKPGL . . . . PVPYMGSPEKTLY . . PNVLVNSWGRI 386
cab10318 (SEQ ID NO: 74) . . GTVILDEGGSSDSSSMIGSKLANLMLTNYSRLSYETHEPYTVSSWCKL 376
cab10319 (SEQ ID NO: 75) . . NEMIKESLQGNTIGQSLLSLMAETVSES . . . . . TEIDRYIMSSWCRK 363
cab40761 (SEQ ID NO: 76) . . DQGYINSYMEALGGSNDGNLPP . . . . . LKELTLISDWTKM 397
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FIG. 6L

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TAX1 (SEQ ID NO: 28) G.FDEVDEGWGNAVSVSPVQQQS..ALAMQNYFLFLKPSKNKPDGIKILM 414
TAX2 (SEQ ID NO: 26) G.FYEADEGWGNAVNVSPMQQQREHELAMQNYFLFLRSAKNMIDGIKILM 410
aab61522 (SEQ ID NO: 64) PVY.EADEGWGKPLWVAS.....ARMS.YKNL..VAFIDTKEGDGIEAWI 300
aab61523 (SEQ ID NO: 62) GLY.DADEGWGKPVWVTG.....RGTSHFKNL..MLLIDTKDGEGIEAWI 408
aab95283 (SEQ ID NO: 63) PMY.DNDEGWGRPVAVRS.....GRSNKFDGKISA.FPGREGNGTVDLEV 459
aab97723 (SEQ ID NO: 64) EMYETADEGWGKPVYAGPI..DLRPTPQVCVLLPQGGVESGNDQSMVVCL 441
aac17079 (SEQ ID NO: 65) PVN.QVDEGWGSPVFGSY.....HFPWGGSAGYVMPMPSSVDDRDWMVYL 544
aac18062 (SEQ ID NO: 66) PLY.EVDEGWGIPSLVDT.....TAVPF...GLIVLMDEAPAGDGIAVRA 412
aac27152 (SEQ ID NO: 67) G.FAEVEYPWGKPKYSCPVVYHRKDI.....VLLFPDIDGDSKGVYYVLA 431
aac99311 (SEQ ID NO: 68) PFY.DVDEGWGKPIWV.C.....LFQPYIKNCVVMMDYPFGDDYGIEAIV 417
aad12025 (SEQ ID NO: 69) P.MYGLDEGWGKEFYTGPGTHDFDGD.....SLILPDQNEDG.SVILAT 433
caa20531 (SEQ ID NO: 70) GWFGSMDEGWNEPVNLRPL.TQRESTVHVGMILKPSKSDPSMEGGVKVIM 435
caa64636 (SEQ ID NO: 71) G.FGEVDEGWGKAVYGGPAKGGVGAIPGVASFYIPFK.NKKGENGIVVPI 424
caa94432 (SEQ ID NO: 72) G.VENVDEGWGKAIFGGPTTTGARITRGLVSFCVPFM.NRNGEKGTALSL 416
cab06427 (SEQ ID NO: 73) P.YQAMDEGWGSPTFFGISNIFYDGQ.....CFLIPSRDGDG.SMTLAI 428
cab10318 (SEQ ID NO: 74) PLY.EASEGWDSPVWVVG.....NVSPVLGNL..AMLIDSKDGQGIEAFV 418
cab10319 (SEQ ID NO: 75) PFY.EVDEGSGSPVWVGY.....ASHTIYDNMVGVVLIDSKEGDGVEAWI 407
cab40761 (SEQ ID NO: 76) P.FHNVGEGNG.....GEPADYMAPLCPPVPQVAYFMKNPKDAKGVLVRI 441
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FIG. 6M

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TAX1 (SEQ ID NO: 28)	F*L**P* L S K*M* K S*F* K I E M E A M M K . K Y V A K V	439
TAX2 (SEQ ID NO: 26)	F*M**P* A S M V K P*F* K I E M E V T I N . K Y V A K I C N S K L	440
aab61522 (SEQ ID NO: ~~64~~)	N*L* D Q N D*M* S R*F* E A D E E L L R Y V S S N P S V M V S V S	331
aab61523 (SEQ ID NO: 62)	T*L* T E E Q*M* S L*F* E C D Q E L L E S A S L N P P V L I	436
aab95283 (SEQ ID NO: 63)	V*L* S P E T*M* A G I E S D G E F M R Y V T N K	482
aab97723 (SEQ ID NO: 64)	C*L**P* P T A V H T*F* T R L L S L N D H K	461
aac17079 (SEQ ID NO: 65)	H*L* T K G Q*L* R F I E E E A S H V L K P I D N D Y L K I	572
aac18062 (SEQ ID NO: 66)	C*L* S E H D*M* I Q*F* Q Q H H Q L L S Y V S	433
aac27152 (SEQ ID NO: 67)	A*L**P* S K E*M* S K*F* Q H W F E D T L C	450
aac99311 (SEQ ID NO: 68)	S*F* E Q E K*M* S A*F* E K N E Q L L Q F V S N	439
aad12025 (SEQ ID NO: 69)	C*L* Q V A H*M* E A*F* K K H F Y E D I	451
caa20531 (SEQ ID NO: 70)	K*L**P* R D A*M* V E*F* K R E M A T M K K L Y F G D T N	461
caa64636 (SEQ ID NO: 71)	C*L**P* G F A*M* E T*F* V K E L D G M L K V D A P L . . V N S N Y A I I R P A L .	460
caa94432 (SEQ ID NO: 72)	C*L**P* P P A*M* E R*F* R A N V H A S L Q V K Q V V D A V D S H M Q T I Q S A S K	455
cab06427 (SEQ ID NO: 73)	N*L* F S S H*L* S R*F* K K Y F Y D F	445
cab10318 (SEQ ID NO: 74)	T*L* P E E N*M* S S*F* E Q N P E L L A F A T M N P S V L V	446
cab10319 (SEQ ID NO: 75)	S*L**P* E E D*M* S V*F* V D D Q E L L A Y A V L N P P V V A	435
cab40761 (SEQ ID NO: 76)	G*L* D P R D V N G*F* S N H F L D C	458

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FIG. 6N